

COPY

(1) GENERAL INFORMATION:

- (i) APPLICANT: CRAIG, NANCY L
- (ii) TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
ATP-DEPENDENT TRANSPOSITION PROTEINS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Anne Brown (Alston & Bird, LLP)
 - (B) STREET: 3605 Glenwood Ave.
 - (C) CITY: Raleigh
 - (D) STATE: NC
 - (E) COUNTRY: USA
 - (F) ZIP: 27608
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Anne
 - (B) REGISTRATION NUMBER: 36,463
 - (C) REFERENCE/DOCKET NUMBER: 5789-3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919 420 2205
 - (B) TELEFAX: 919 881 3175

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1668
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGT GCT ACC CGG ATT CAA GCA GTT TAT CGT GAT ACG GGG GTA GAG Met Ser Ala Thr Arg Ile Gln Ala Val Tyr Arg Asp Thr Gly Val Glu 1 5 10 15	48
GCT TAT CGT GAT AAT CCT TTT ATC GAG GCC TTA CCA CCA TTA CAA GAG Ala Tyr Arg Asp Asn Pro Phe Ile Glu Ala Leu Pro Pro Leu Gln Glu 20 25 30	96
TCA GTG AAT AGT GCT GCA TCA CTG AAA TCC TCT TTA CAG CTT ACT TCC Ser Val Asn Ser Ala Ala Ser Leu Lys Ser Ser Leu Gln Leu Thr Ser 35 40 45	144
TCT GAC TTG CAA AAG TCC CGT GTT ATC AGA GCT CAT ACC ATT TGT CGT Ser Asp Leu Gln Lys Ser Arg Val Ile Arg Ala His Thr Ile Cys Arg 50 55 60	192
ATT CCA GAT GAC TAT TTT CAG CCA TTA GGT ACG CAT TTG CTA CTA AGT Ile Pro Asp Asp Tyr Phe Gln Pro Leu Gly Thr His Leu Leu Leu Ser 65 70 75 80	240
GAG CGT ATT TCG GTC ATG ATT CGA GGT GGC TAC GTA GGC AGA AAT CCT Glu Arg Ile Ser Val Met Ile Arg Gly Gly Tyr Val Gly Arg Asn Pro 85 90 95	288
AAA ACA GGA GAT TTA CAA AAG CAT TTA CAA AAT GGT TAT GAG CGT GTT Lys Thr Gly Asp Leu Gln Lys His Leu Gln Asn Gly Tyr Glu Arg Val 100 105 110	336
CAA ACG GGA GAG TTG GAG ACA TTT CGC TTT GAG GAG GCA CGA TCT ACG Gln Thr Gly Glu Leu Glu Thr Phe Arg Phe Glu Glu Ala Arg Ser Thr 115 120 125	384
GCA CAA AGC TTA TTG TTA ATT GGT TGT TCT GGT AGT GGG AAG ACG ACC Ala Gln Ser Leu Leu Leu Ile Gly Cys Ser Gly Ser Gly Lys Thr Thr 130 135 140	432
TCT CTT CAT CGT ATT CTA GCC ACG TAT CCT CAG GTG ATT TAC CAT CGT Ser Leu His Arg Ile Leu Ala Thr Tyr Pro Gln Val Ile Tyr His Arg 145 150 155 160	480
GAA CTC AAT GTA GAG CAG GTG GTG TAT TTG AAA ATA GAC TGC TCG CAT Glu Leu Asn Val Glu Gln Val Val Tyr Leu Lys Ile Asp Cys Ser His 165 170 175	528
AAT GGT TCG CTA AAA GAA ATC TGC TTG AAT TTT TTC AGA GCG TTG GAT Asn Gly Ser Leu Lys Glu Ile Cys Leu Asn Phe Phe Arg Ala Leu Asp 180 185 190	576
CGA GCC TTG GGC TCG AAC TAT GAG CGT CGT TAT GGC TTA AAA CGT CAT Arg Ala Leu Gly Ser Asn Tyr Glu Arg Arg Tyr Gly Leu Lys Arg His 195 200 205	624
GGT ATA GAA ACC ATG TTG GCT TTG ATG TCG CAA ATA GCC AAT GCA CAT Gly Ile Glu Thr Met Leu Ala Leu Met Ser Gln Ile Ala Asn Ala His 210 215 220	672
GCT TTA GGG TTG TTG GTT ATT GAT GAA ATT CAG CAT TTA AGC CGC TCT	720

Ala Leu Gly Leu Leu Val Ile Asp Glu Ile Gln His Leu Ser Arg Ser	
225 230 235 240	
CGT TCG GGT GGA TCT CAA GAG ATG CTG AAC TTT TTT GTG ACG ATG GTG	768
Arg Ser Gly Gly Ser Gln Glu Met Leu Asn Phe Phe Val Thr Met Val	
245 250 255	
AAT ATT ATT GGC GTA CCA GTG ATG TTG ATT GGT ACC CCT AAA GCA CGA	816
Asn Ile Ile Gly Val Pro Val Met Leu Ile Gly Thr Pro Lys Ala Arg	
260 265 270	
GAG ATT TTT GAG GCT GAT TTG CGG TCT GCA CGT AGA GGG GCA GGG TTT	864
Glu Ile Phe Glu Ala Asp Leu Arg Ser Ala Arg Arg Gly Ala Gly Phe	
275 280 285	
GGG GCT ATA TTC TGG GAT CCT ATA CAA CAA ACG CAA CGT GGA AAG CCC	912
Gly Ala Ile Phe Trp Asp Pro Ile Gln Gln Thr Gln Arg Gly Lys Pro	
290 295 300	
AAT CAA GAG TGG ATC GCT TTT ACG GAT AAT CTT TGG CAA TTA CAG CTT	960
Asn Gln Glu Trp Ile Ala Phe Thr Asp Asn Leu Trp Gln Leu Gln Leu	
305 310 315 320	
TTA CAA CGC AAA GAT GCG CTG TTA TCG GAT GAG GTC CGT GAT GTG TGG	1008
Leu Gln Arg Lys Asp Ala Leu Leu Ser Asp Glu Val Arg Asp Val Trp	
325 330 335	
TAT GAG CTA AGC CAA GGA GTG ATG GAC ATT GTA GTA AAA CTT TTT GTA	1056
Tyr Glu Leu Ser Gln Gly Val Met Asp Ile Val Val Lys Leu Phe Val	
340 345 350	
CTC GCT CAG CTC CGT GCG CTA GCT TTA GGC AAT GAG CGT ATT ACC GCT	1104
Leu Ala Gln Leu Arg Ala Leu Ala Leu Gly Asn Glu Arg Ile Thr Ala	
355 360 365	
GGT TTA TTG CGG CAA GTG TAT CAA GAT GAG TTA AAG CCT GTG CAC CCC	1152
Gly Leu Leu Arg Gln Val Tyr Gln Asp Glu Leu Lys Pro Val His Pro	
370 375 380	
ATG CTA GAG GCA TTA CGC TCG GGT ATC CCA GAA CGC ATT GCT CGT TAT	1200
Met Leu Glu Ala Leu Arg Ser Gly Ile Pro Glu Arg Ile Ala Arg Tyr	
385 390 395 400	
TCT GAT CTA GTC GTT CCC GAG ATT GAT AAA CGG TTA ATC CAA CTT CAG	1248
Ser Asp Leu Val Val Pro Glu Ile Asp Lys Arg Leu Ile Gln Leu Gln	
405 410 415	
CTA GAT ATC GCA GCG ATA CAA GAA CAA ACA CCA GAA GAA AAA GCC CTT	1296
Leu Asp Ile Ala Ala Ile Gln Glu Gln Thr Pro Glu Glu Lys Ala Leu	
420 425 430	
CAA GAG TTA GAT ACC GAA GAT CAG CGT CAT TTA TAT CTG ATG CTG AAA	1344
Gln Glu Leu Asp Thr Glu Asp Gln Arg His Leu Tyr Leu Met Leu Lys	
435 440 445	
GAG GAT TAC GAT TCA AGC CTG TTA ATT CCC ACT ATT AAA AAA GCG TTT	1392
Glu Asp Tyr Asp Ser Ser Leu Leu Ile Pro Thr Ile Lys Lys Ala Phe	
450 455 460	

AGC CAG AAT CCA ACG ATG ACA AGA CAA AAG TTA CTG CCT CTT GTT TTG 1440
 Ser Gln Asn Pro Thr Met Thr Arg Gln Lys Leu Leu Pro Leu Val Leu
 465 470 475 480

CAG TGG TTG ATG GAA GGC GAA ACG GTA GTG TCA GAA CTA GAA AAG CCC 1488
 Gln Trp Leu Met Glu Gly Glu Thr Val Val Ser Glu Leu Glu Lys Pro
 485 490 495

TCC AAG AGT AAA AAG GTT TCG GCT ATA AAG GTA GTC AAG CCC AGC GAC 1536
 Ser Lys Ser Lys Lys Val Ser Ala Ile Lys Val Val Lys Pro Ser Asp
 500 505 510

TGG GAT AGC TTG CCT GAT ACG GAT TTA CGT TAT ATC TAT TCA CAA CGC 1584
 Trp Asp Ser Leu Pro Asp Thr Asp Leu Arg Tyr Ile Tyr Ser Gln Arg
 515 520 525

CAA CCT GAA AAA ACC ATG CAT GAA CGG TTA AAA GGG AAA GGG GTA ATA 1632
 Gln Pro Glu Lys Thr Met His Glu Arg Leu Lys Gly Lys Gly Val Ile
 530 535 540

GTG GAT ATG GCG AGC TTA TTT AAA CAA GCA GGT TAG CC 1670
 Val Asp Met Ala Ser Leu Phe Lys Gln Ala Gly *
 545 550 555

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Thr Arg Ile Gln Ala Val Tyr Arg Asp Thr Gly Val Glu
 1 5 10 15
 Ala Tyr Arg Asp Asn Pro Phe Ile Glu Ala Leu Pro Pro Leu Gln Glu
 20 25 30
 Ser Val Asn Ser Ala Ala Ser Leu Lys Ser Ser Leu Gln Leu Thr Ser
 35 40 45
 Ser Asp Leu Gln Lys Ser Arg Val Ile Arg Ala His Thr Ile Cys Arg
 50 55 60
 Ile Pro Asp Asp Tyr Phe Gln Pro Leu Gly Thr His Leu Leu Leu Ser
 65 70 75 80
 Glu Arg Ile Ser Val Met Ile Arg Gly Gly Tyr Val Gly Arg Asn Pro
 85 90 95
 Lys Thr Gly Asp Leu Gln Lys His Leu Gln Asn Gly Tyr Glu Arg Val
 100 105 110

Gln Thr Gly Glu Leu Glu Thr Phe Arg Phe Glu Glu Ala Arg Ser Thr
 115 120 125
 Ala Gln Ser Leu Leu Leu Ile Gly Cys Ser Gly Ser Gly Lys Thr Thr
 130 135 140
 Ser Leu His Arg Ile Leu Ala Thr Tyr Pro Gln Val Ile Tyr His Arg
 145 150 155 160
 Glu Leu Asn Val Glu Gln Val Val Tyr Leu Lys Ile Asp Cys Ser His
 165 170 175
 Asn Gly Ser Leu Lys Glu Ile Cys Leu Asn Phe Phe Arg Ala Leu Asp
 180 185 190
 Arg Ala Leu Gly Ser Asn Tyr Glu Arg Arg Tyr Gly Leu Lys Arg His
 195 200 205
 Gly Ile Glu Thr Met Leu Ala Leu Met Ser Gln Ile Ala Asn Ala His
 210 215 220
 Ala Leu Gly Leu Leu Val Ile Asp Glu Ile Gln His Leu Ser Arg Ser
 225 230 235 240
 Arg Ser Gly Gly Ser Gln Glu Met Leu Asn Phe Phe Val Thr Met Val
 245 250 255
 Asn Ile Ile Gly Val Pro Val Met Leu Ile Gly Thr Pro Lys Ala Arg
 260 265 270
 Glu Ile Phe Glu Ala Asp Leu Arg Ser Ala Arg Arg Gly Ala Gly Phe
 275 280 285
 Gly Ala Ile Phe Trp Asp Pro Ile Gln Gln Thr Gln Arg Gly Lys Pro
 290 295 300
 Asn Gln Glu Trp Ile Ala Phe Thr Asp Asn Leu Trp Gln Leu Gln Leu
 305 310 315 320
 Leu Gln Arg Lys Asp Ala Leu Leu Ser Asp Glu Val Arg Asp Val Trp
 325 330 335
 Tyr Glu Leu Ser Gln Gly Val Met Asp Ile Val Val Lys Leu Phe Val
 340 345 350
 Leu Ala Gln Leu Arg Ala Leu Ala Leu Gly Asn Glu Arg Ile Thr Ala
 355 360 365
 Gly Leu Leu Arg Gln Val Tyr Gln Asp Glu Leu Lys Pro Val His Pro
 370 375 380
 Met Leu Glu Ala Leu Arg Ser Gly Ile Pro Glu Arg Ile Ala Arg Tyr
 385 390 395 400
 Ser Asp Leu Val Val Pro Glu Ile Asp Lys Arg Leu Ile Gln Leu Gln
 405 410 415
 Leu Asp Ile Ala Ala Ile Gln Glu Gln Thr Pro Glu Glu Lys Ala Leu

[illegible]

Year	Population	GDP	Exports	Imports	Balance of Trade
1980	100	100	100	100	0
1981	100	100	100	100	0
1982	100	100	100	100	0
1983	100	100	100	100	0
1984	100	100	100	100	0
1985	100	100	100	100	0
1986	100	100	100	100	0
1987	100	100	100	100	0
1988	100	100	100	100	0
1989	100	100	100	100	0
1990	100	100	100	100	0
1991	100	100	100	100	0
1992	100	100	100	100	0
1993	100	100	100	100	0
1994	100	100	100	100	0
1995	100	100	100	100	0
1996	100	100	100	100	0
1997	100	100	100	100	0
1998	100	100	100	100	0
1999	100	100	100	100	0
2000	100	100	100	100	0
2001	100	100	100	100	0
2002	100	100	100	100	0
2003	100	100	100	100	0
2004	100	100	100	100	0
2005	100	100	100	100	0
2006	100	100	100	100	0
2007	100	100	100	100	0
2008	100	100	100	100	0
2009	100	100	100	100	0
2010	100	100	100	100	0
2011	100	100	100	100	0
2012	100	100	100	100	0
2013	100	100	100	100	0
2014	100	100	100	100	0
2015	100	100	100	100	0
2016	100	100	100	100	0
2017	100	100	100	100	0
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2019	100	100	100	100	0
2020	100	100	100	100	0
2021	100	100	100	100	0
2022	100	100	100	100	0
2023	100	100	100	100	0
2024	100	100	100	100	0
2025	100	100	100	100	0
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2027	100	100	100	100	0
2028	100	100	100	100	0
2029	100	100	100	100	0
2030	100	100	100	100	0
2031	100	100	100	100	0
2032	100	100	100	100	0
2033	100	100	100	100	0
2034	100	100	100	100	0
2035	100	100	100	100	0
2036	100	100	100	100	0
2037	100	100	100	100	0
2038	100	100	100	100	0
2039	100	100	100	100	0
2040	100	100	100	100	0
2041	100	100	100	100	0
2042	100	100	100	100	0
2043	100	100	100	100	0
2044	100	100	100	100	0
2045	100	100	100	100	0
2046	100	100	100	100	0
2047					

Parameter	Unit	Value
Temperature	°C	25
Pressure	atm	1
Time	h	24
Concentration	mol/L	0.1
Volume	L	1
Mass	g	10
Length	cm	10
Area	cm ²	100
Volume	cm ³	1000
Mass	kg	1000
Length	m	100
Area	m ²	10000
Volume	m ³	1000000
Mass	ton	1000
Length	km	1000
Area	km ²	1000000
Volume	km ³	1000000000
Mass	g	0.001
Length	mm	0.001
Area	mm ²	0.000001
Volume	mm ³	0.000001
Mass	mg	0.001
Length	μm	0.000001
Area	μm ²	0.000001
Volume	μm ³	0.000001
Mass	μg	0.000001
Length	nm	0.000000001
Area	nm ²	0.000000001
Volume	nm ³	0.000000001
Mass	ng	0.000000001
Length	pm	0.000000000001
Area	pm ²	0.000000000001
Volume	pm ³	0.000000000001
Mass	pg	0.000000000001
Length	fm	0.000000000000001
Area	fm ²	0.000000000000001
Volume	fm ³	0.000000000000001
Mass	fg	0.000000000000001

Parameter	Unit	Value
Temperature	°C	25
Pressure	atm	1
Time	h	24
Concentration	mol/L	0.1
Volume	L	1
Mass	g	10
Length	cm	10
Area	cm ²	100
Volume	cm ³	1000
Mass	kg	1000
Length	m	100
Area	m ²	10000
Volume	m ³	1000000
Mass	ton	1000
Length	km	1000
Area	km ²	1000000
Volume	km ³	1000000000
Mass	g	0.001
Length	mm	0.001
Area	mm ²	0.000001
Volume	mm ³	0.000001
Mass	mg	0.001
Length	μm	0.000001
Area	μm ²	0.000001
Volume	μm ³	0.000001
Mass	μg	0.000001
Length	nm	0.000000001
Area	nm ²	0.000000001
Volume	nm ³	0.000000001
Mass	ng	0.000000001
Length	pm	0.000000000001
Area	pm ²	0.000000000001
Volume	pm ³	0.000000000001
Mass	pg	0.000000000001
Length	fm	0.000000000000001
Area	fm ²	0.000000000000001
Volume	fm ³	0.000000000000001
Mass	fg	0.000000000000001

TTTGC GTATT GGGCGCCAGG GTGGTTTTTC TTTTCACCAG TGAGACGGGC AACAGCTGAT 540

TGCCCTTCAC CGCCTGGCCC TGAGAGAGTT GCAGCAAGCG GTCCACGCTG GTTTGCCCCA 600

GCAGGCGAAA ATCCTGTTTG ATGGTGGTTG ACGGCGGGAT ATAACATGAG CTGTCTTCGG 660

TATCGTCGTA TCCCACTACC GAGATATCCG CACCAACGCG CAGCCCGGAC TCGGTAATGG 720

CGCGCATTCG GCCCAGCGCC ATCTGATCGT TGGCAACCAG CATCGCAGTG GGAACGATGC 780

CCTCATTCAG CATTTGCATG GTTTGTTGAA AACCGGACAT GGCACTCCAG TCGCCTTCCC 840

GTTCCGCTAT CGGCTGAATT TGATTGCGAG TGAGATATTT ATGCCAGCCA GCCAGACGCA 900

GACGCGCCGA GACAGAACTT AATGGGCCCC CTAACAGCGC GATTTGTCTG TGACCCAATG 960

CGACCAGATG CTCACGCCC AGTCGCGTAC CGTCTTCAAT GGAGAAAATA ATACTGTTGA 1020

TGGTGTCTG GTCAGAGACA TCAAGAAATA ACGCCGGAAC ATTAGTGCAG GCAGCTTCCA 1080

CAGCAATGGC ATCCTGTGTA TCCAGCGGAT AGTTAATGAT CAGCCCACTG ACGCGTTGCG 1140

CGAGAAGATT GTGCACCGCC GCTTTACAGG CTTGCGAGCC GCTTCGTCTT ACCATCGACA 1200

CCACCACGCT GGCACCCAGT TGATCGGCGC GAGATTTAAT CGCCGCGACA ATTTGCGACG 1260

GCGCGTGCAG GGCCAGACTG GAGGTGGCAA CGCCAATCAG CAACGACTGT TTGCCCGCCA 1320

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CCC CGTTTT CGCAGAAACG TGGCTGGCCT GGTTCACCAC GCGGGAACG GTCTGATAAG 1440

AGACACCGGC ATACTCTGCG ACATCGTATA ACGTTACTGG TTTACATTG ACCACCTGA 1500

ATTGACTCTC TTCCGGGCGC TATCATGCCA TACCGGAAA GGTTTTGCAC CATTCGATGG 1560

TGTCAACGTA AATGCATGCC GCTTCGCCTT CGCGCGGAA TTGATCTGCT GCCTCGCGCG 1620

TTTCGGTGAT GACGTTGAAA ACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG 1680

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AGATGCGTAA GGAGAAAATA CCGCATCAGG CGCTCTTCCG CTTCTCTGCT CACTGACTCG 1920

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ACCGGATACC TGTCCGCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC 2280
 TGTAGGTATC TCAGTTGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC 2340
 CCCGTTACGC CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA 2400
 AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT 2460
 GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA 2520
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 TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTGCTAA GCAGCAGATT 2640
 ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT 2700
 CAGTGAAGC AAAACTCAGC TTAAGGGATT TTGGTCATGA GATTATCAA AAGATCTTC 2760
 ACCTAGATCC TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAGTAT ATATGAGTAA 2820
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 CCGCTGTGTA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT 3600
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CGGCCAAAAC AGCCAAGCTT GCATGCCTGC AGGTCGACTC TAGAGGATCC CCAAGAAAGT 4260
CCGTCGGACA GCTTTAATAA ACCCTGCACT TATCTGTTTA GTGTGGGCGG ACAAATAGT 4320
TGGGAAC TGG GAGGGGTGGA AATGGAGTTT TTAAGGATTA TTTAGGGAAG AGTGACAAA 4380
TAGATGGGAA CTGGGTGTAG CGTCGTAAGC TAATACGAAA ATTAATAATG ACAAATAGT 4440
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AAACGCTCTG CTCGAGGCCG CGATTAAAT CCAACATGGA TGCTGATTTA TATGGGTATA 4680
AATGGGCTCG CGATAATGTC GGGCAATCAG GTGCGACAAT CTATCGATTG TATGGGAAGC 4740
CCGATGCGCC AGAGTTGTTT CTGAAACATG GCAAAGGTAG CGTTGCCAAT GATGTTACAG 4800
ATGAGATGGT CAGACTAAAC TGGCTGACGG AATTTATGCC TCTTCCGACC ATCAAGCATT 4860
TTATCCGTAC TCCTGATGAT GCATGGTTAC TCACCACTGC GATCCCCGGG AAAACAGCAT 4920
TCCAGGTATT AGAAGAATAT CCTGATTCAG GTGAAAATAT TGTGTAGTCG CTGGCAGTGT 4980
TCCTGCGCCG GTTGCAATTCG ATTCTGTTT GTAATTGTCC TTTTAACAGC GATCGCGTAT 5040
TTCGCTCTCG TCAGGCGCAA TCACGAATGA ATAACGGTTT GGTGTAGTCG AGTGATTTTG 5100
ATGACGAGCG TAATGGCTGG CCTGTTGAAC AAGTCTGGAA AGAATGCAT AAGCTTTTGC 5160
CATTCTCACC GGATTCAGTC GTCACCTCATG GTGATTCTC ACTTGATAAC CTTATTTTGT 5220
ACGAGGGGAA ATTAATAGGT TGTATTGATG TTGACGAGT CGGAATCGCA GACCGATACC 5280
AGGATCTTGC CATCCTATGG AACTGCCTCG GTGAGTTTTC TCCTTCATTA CAGAAACGGC 5340
TTTTTCAAAA ATATGGTATT GATAATCCTG ATATGAATAA ATTGCAGTTT CATTTGATGC 5400
TCGATGAGTT TTTCTAATCA GAATTGGTTA ATTGGTTGTA ACACTGGCAG AGCATTACGC 5460
TGACTTGACG GGACGGCGGC TTTGTTGAAT AAATCGAACT TTTGCTGAGT TGAAGGATCA 5520
GATCACGCAT CTTCCCGACA ACGCAGACCG TTCCGTGGCA AAGCAAAAGT TCAAAATCAC 5580
CAACTGGTCC ACCTACAACA AAGCTCTCAT CAACCGTGGC TCCCTCACTT TCTGGCTGGA 5640
TGATGGGGCG ATTCAGGCCT GGTATGAGTC AGCAACACCT TCTTCACGAG GCAGACCTCA 5700

GCGCCCCCCC CCCCCTGCAG GTCGACCCCA CGCCCCCTCTT TAATACGACG GGCAATTGTC 5760
 ACTTCAGAAA ATGAAGAGTT TGCTTTAGCC ATAACAAAAG TCCAGTATGC TTTTTCACAG 5820
 CATAACTGGA CTGATTTTCAG TTACAACATA TTCTGTCTAG TTTAAGACTT TATGTGCATA 5880
 GTTTAGATCT ATTTTGTTC A GTTTAAGACT TTATTGTCCG CCCACA 5926

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "pEM-delta"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGATCAATT CGCGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCGC TTTCCAGTCG 60
 GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG 120
 CGTATTGGGC GCCAGGGTGG TTTTCTTTT CACCACTGAG ACGGGCAACA GCTGATTGCC 180
 CTTACCCGCG TGCCCTGAG AGAGTTGCAG CAAGCGGTCC ACGCTGGTTT GCCCCAGCAG 240
 GCGAAAATCC TGTTTGATGG TGGTTGACGG CGGGATATAA CATGAGCTGT CTTGGGTATC 300
 GTCGTATCCC ACTACCGAGA TATCCGCACC AACGCGCAGC CCGGACTCGG TAATGGGGCG 360
 CATTGCGCCC AGCGCCATCT GATCGTTGGC AACCAGCATC GCAGTGGGAA CGATGCCCTC 420
 ATTCAGCATT TGCGATGGTT GTTGA AAACC GGACATGGCA CTCAGTCGC CTTCGCCGTT 480
 CGCTATCGCG TGAATTTGAT TGCGAGTGAG ATATTATGC CAGCCAGCCA GACGCAGACG 540
 CGCCGAGACA GAACTTAATG GGCCCGCTAA CAGCGCGATT TGCTGGTGAC CCAATGCGAC 600
 CAGATGCTCC ACGCCAGTC GCGTACCGTC TTCATGGGAG AAAATAATAC TGTGATGGG 660
 TGTCTGGTCA GAGACATCAA GAAATAACGC CGGAACATTA GTGCAGGCAG CTTCACAGC 720
 AATGGCATCC TGATCATCCA GCGGATAGTT AATGATCAGC CCACTGACGC GTTGC GCGAG 780
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 CACGCTGGCA CCCAGTTGAT CGGCGCGAGA TTTAATCGCC GCGACAATTT GCGACGGGCG 900
 GTGCAGGGCC AGACTGGAGG TGGCAACGCC AATCAGCAAC GACTGTTTGC CCGCCAGTTG 960
 TTGTGCCACG CGGTTGGGAA TGTAATTCAG CTCGCCATC GCGCGTTCCA CTTTTTCCCG 1020

CGTTTTCGCA GAAACGTGGC TGGCCTGGTT CACCACGCGG GAAACGTCT GATAAGAGAC 1080

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 TCGCGCAGAG TTGTTTCTGA AACATGGCAA AGGTAGCGTT GCCAATGATG TTACAGATGA 4440
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 CACACATAT ACGAGCCGGA TGATTAATTG TCAACAGCTC ATTTCAGAAAT ATTTGCCAGA 5760
 ACCGTTATGA TGTGCGCGCA AAAACATTA TCCAGAACGG GAGTGC GCCT TGAGCGACAC 5820
 GAATTATGCA GTGATTTACG ACCTGCACAG CCATACCACA GCTTCCGATG GCTGCCTGAC 5880
 GCCAGAAGCA TTGGTGACCC GTGCAGTCGA TGATAAGCTG TCAAAAC 5926

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "pER183 (target plasmid)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATAGGTACAT	TGAGCAACTG	ACTGAAATGC	CTCAAAATGT	TCTTTACGAT	GCCATTGGGA	180
TATATCAACG	TGGTATATC	CAGTGATTTT	TTTCTCCATT	TTAGCTTCCT	TAGCTCCTGA	240
AAATCTCGAT	AACTCAAAAA	ATACGCCCGG	TAGTGATCTT	ATTTTCATTAT	GGTGAAAGTT	300
GGAACCTCTT	ACGTGCCGAT	CAACGTCTCA	TTTTCGCCAA	AAGTTGGCCC	AGGGCTTCCC	360
GGTATCAACA	GGGACACCAG	GATTTATTTA	TTCTGCGAAG	TGATCTTCCG	TCACAGGTAT	420
TTATTCGGCG	CAAAAGTCGT	CGGGTGATGC	TGCCAACTTA	CTGATTTAGT	GTATGATGGT	480
GTTTTTGAGG	TGCTCCAGTG	GCTTCTGTTT	CTATCAGCTG	TCCCTCCTGT	TCAGCTACTG	540
ACGGGGTGGT	GCGTAACGGC	AAAAGCACCG	CCGGACATCA	GCGCTAGCGG	AGTGATATACT	600
GGCTTACTAT	GTTGGCACTG	ATGAGGGTGT	CAGTGAAGTG	CTTCATGTGG	CAGGAGAAAA	660
AAGGCTGCAC	CGGTGCGTCA	GCAGAATATG	TGATACAGGA	TATATTCCCG	TTCTCGCTC	720
ACTGACTCGC	TACGCTCGGT	CGTTCGACTG	CGGCGAGCGG	AAATGGCTTA	CGAACGGGGC	780
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AGCCGTTTTT	CCATAGGCTC	CGCCCCCTG	ACAAGCATCA	CGAAATCTGA	CGCTCAAATC	900
AGTGGTGGCG	AAACCCGACA	GGACTATAAA	GATACCAGGC	GTTTCCCCTG	GCGGCTCCCT	960
CGTGCGCTCT	CCTGTTCTGT	CCTTTCGGTT	TACCGGTGTC	ATTCCGCTGT	TATGGCCGCG	1020
TTTGTCTCAT	TCCACGCTGT	ACACTCAGTT	CCGGGTAGGC	AGTTCGCTCC	AAGCTGGACT	1080
GTATGCACGA	ACCCCCCGTT	CAGTCCGACC	GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	1140
AGTCCAACCC	GGAAAGACAT	GCAAAAGCAC	CACTGGCAGC	AGCCACTGGT	AATTGATTTA	1200
GAGGAGTTAG	TCTTGAAGTC	ATGCGCCGGT	TAAGGCTAAA	CTGAAAGGAC	AAGTTTTGGT	1260
GACTGCGCTC	CTCCAAGCCA	GTTACCTCGG	TTCAAAGAGT	TGTTAGCTCA	GAGAACCCTT	1320
GAAAAACCGC	CCTGCAAGGC	GGTTTTTTCG	TTTTCAGAGC	AAGAGATTAC	GCGCAGACCA	1380
AAACGATCTC	AAGAAGATCA	TCTTATTAAT	CAGATAAAAT	ATTTCTAGAT	TTCAGTGCAA	1440
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GCAATTTCTA TCGCGACCCG TTCTCGGAGC ACTGTCCGAC CGCTTTGGCC GCCGCCCAGT 2280

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TATCATGCAA CTCGTAGGAC AGGTGCCGGC AGCGCTCTGG GTCATTTTTCG GCGAGGACCG 6960
CTTTCGCTGG AGCGCGACGA TGATCGGCCT GTCGCTTGCG GTATTTCGGAA TCTTGACGCG 7020
CCTCGCTCAA GCCTTCTGTA CTGTGCCCGC CACCAAACGT TTCGGCGAGA AGCAGGCCAT 7080
TATCGCCGGC ATGGCGGCCG ACGCGCTGGG CTACGTCTTG CTGGCGTTTCG CGACGCGAGG 7140
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CCTACGTGCT GCTGAAGTTG CCCGCAACAG AGAGTGAAC CAACCGGTGA TACCACGATA 7860
CTATGACTGA GAGTCAACGC CATGAGCGGC CTCATTCTT ATTCTGAGTT ACAACAGTCC 7920
GCACCGCTGC CGGTAGCTCC TTCCGTTGGG CGCGGGGCAT GACTATCGTC GCCGCACTTA 7980
TGACTGTCTT CTTTATCATG CAATCGTAG GACAGGTGCC GGCAGCGCCC AACAGTCCCC 8040
CGGCCACGGG GCCTGCCACC ATACCCACGC CGAAACAAGC GCCCTGCACC ATTATGTTCC 8100
GGATCTGCAT CGCAGGATGC TGCTGGCTAC CCTGTGGAAC ACCTACATCT GTATTAACGA 8160
AGCGCTAACC GTTTTATCA GGCTCTGGGA GGCAGAATAA ATGATCATAT CGTCAATTAT 8220
TACCTCCACG GGGAGAGCCT GAGCAAACGT GCCTCAGGCA TTTGAGAAGC ACACGGTCAC 8280
ACTGCTCCG GTAGTCAATA AACCGTAAA CCAGCAATAG ACATAAGCGG CTATTTAACG 8340
ACCTGCGCCT GAACCGACGA CCGGTCGAA TTTGCTTTCG AATTCTGCGC ATTCATCCGC 8400
TTATTATCAC TTATTCAGGC GTAGCAACCA GCGGTTTAAG GGCACCAATA ACTGCCTTAA 8460
AAAAATTACG CCCCGCCCTG CCACTCATCG CAGTACTGTT GTAATTCATT AAGCATTCTG 8520

CCGACATGGA AGCCATCACA GACGGCATGA TGAACCTGAA TCGCCAGCGG CATCAGCACC 8580
 TTGTGCGCCTT GCGTATAATA TTTGCCCATG GTGAAAACGG GGGCGAAGAA GTTGTCCATA 8640
 TTGGCCACGT TTAAATCAAA ACTGGTGAAA CTCACCCAGG GATTGGCTGA GACGAAAAAC 8700
 ATATTCTCAA TAAACCCCTT AGGGAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT 8760
 TCGCAATATA TGTGTAGAAA CTGCCGGAAT TCGTCGTGTT ATTCACTCCA GAGCGATGAA 8820
 AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC CCATATCACC 8880
 AGCTCACCGT CTTTCATTGC CATACG 8906

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "pRM2 (target plasmid)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGCCCAATA CGCAAACCGC CTCTCCCCGC GCGTTGGCCG ATTCATTAAT GCAGCTGGCA 60
 CGACAGGTTT CCGACTGGA AAGCGGGCAG TGAGCGCAAC GCAATTAATG TGAGTTAGCT 120
 CACTCATTAG GCACCCACAG CTTTACACTT TATGCTTCCG GCTCGTATGT TGTGTGGAAT 180
 TGTGAGCGGA TAACAATTC ACACAGGAAA CAGCTATGAC CATGATTACG AATTCGAGCT 240
 CGGTACCCGG GGATCCTCTA GAGTCGAGAT GCCGCATGTG GAAGAGGTGA TTGCACCGAT 300
 CTCTCTACAC GTTCCGCTGC AGCTGCTGGC TTACCATGTC GCGCTGATCA AAGGCACCGA 360
 CGTTGACCAG CCGCGTAACC TGGCAAAATC GGTACGGTT GAGTAATAAA TGGATGCCCT 420
 GCGTAAGCGG GGCAATTTTC TTCTGTTTAT GTTTTAAATC AAACATCCTG CCAACTCCAT 480
 GTGACAAACC GTCATCTTCG GCTACTTTTT CTCTGTCACA GAATGAAAAT TTTCTGTCTAT 540
 CTCTTCGTGA TTAATGTTTG TAATTGACTG AATATCAACG CTTATTTAAA TCAGACTGAA 600
 GACTTATCTC TCCTGTCTAT AAAACTGTCA TATTCCTTAC ATATAACTGT CACCTGTTTG 660
 TCCTATTTTG CTGTCTGAG CCAACAAACA ATGCTTTATG AATCTCTCCA GGAGACATTA 720
 TGAAGATTAT GCGTACCACC GTCGCAACTG TTGTCGCCGC GACCTTATCG ACCTGCAGGC 780
 ATGCAAGCTT GGCAGTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAA CCTGCGCTTA 840

CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG 900
 CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCCTGATGC 960
 GGTATTTTCT CTTTACGCAT CTGTGCGGTA TTTCACACCG CATATGGTGC ACTCTCAGTA 1020
 CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA CCGCCCAACA CCCGTGACG 1080
 CGCCCTGACG GGCTTGTCTG CTCCCCGGCAT CCGCTTACAG ACAAGCTGTG ACCGTCTCCG 1140
 GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCAGAA ACGCGCGAGA CGAAAGGGCC 1200
 TCGTGATACG CCTATTTTAA TAGGTTAATG TCATGATAAT AATGGTTTCT TAGACGTCAG 1260
 GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTGG TTTATTTTTC TAAATACATT 1320
 CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA 1380
 GGAAGAGTAT GAGTATTTCA CATTTCGGTG TCGCCCTTAT TCCCTTTTTT GCGGCATTTT 1440
 GCCTTCTGT TTTTGCTCAC CCGAAACGC TGGTGAAAGT AAAAGATGCT GAAGATCAGT 1500
 TGGGTGCACG AGTGGGTTAC ATCGAACTGG ATCTCAACAG CGGTAAGATC CTTGAGAGTT 1560
 TTCGCCCGCA AGAAGCTTTT CCAATGATGA GCACTTTTAA AGTTCTGCTA TGTGGCGCGG 1620
 TATTATCCCG TATTGACGCC GGGCAAGAGC AACTCGGTG CCGCATACAC TATTCTCAGA 1680
 ATGACTTGTT TGAGTACTCA CCACTCAGC AAAAGCATCT TACGGATGGC ATGACAGTAA 1740
 GAGAATTATG CAGTGTGACC ATAACCATGA GTGATAACAC TCGCGCCAAC TTACTTCTGA 1800
 CAACGATCGG AGGACCGAAG GAGCTAACCG CTTTTTTGCA CAACATGGGG GATCATGTAA 1860
 CTCGCCCTGA TCGTTGGGAA CCGGAGCTGA ATGAAGCCAT ACCAAACGAC GAGCGTGACA 1920
 CCACGATGCC TGTAGCAATG GCAACAACGT TGCGCAAACT ATTAAGTGGC GAACTACTTA 1980
 CTCTAGCTTC CCGGCAACAA TTAATAGACT GGATGGAGGC GGATAAAGTT GCAGGACCAC 2040
 TTCTGCGCTC GGCCCTTCCG GCTGGCTGGT TTATTGCTGA TAAATCTGGA GCCCGTGAGC 2100
 GTGGGTCTCG CGGTATCATT GCAGCACTGG GGCCAGATGG TAAGCCCTCC CGTATCGTAG 2160
 TTATCTACAC GACGGGGAGT CAGGCAACTA TGGATGAACG AAATAGACAG ATCGCTGAGA 2220
 TAGGTGCCTC ACTGATTAAG CATTGGTAAC TGTGAGACCA AGTTTACTCA TATATACTTT 2280
 AGATTGATTT AAAAATTCAT TTTTAAATTA AAAGGATCTA GGTGAAGATC CTTTTTGATA 2340
 ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGACGCTCA GACCCCGTAG 2400
 AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTCTGCG CGTAATCTGC TGCTTGCAAA 2460
 CAAAAAACC ACCGCTACCA GCGGTGGTGT GTTTGCCGGA TCAAGAGCTA CCAACTCTTT 2520
 TTCGAAGGT AACTGGCTTC AGCAGAGCGC AGATACCAAA TACTGTCTCT CTAGTGTAGC 2580

CGTAGTTAGG CCACCACTTC AAGAACTCTG TAGCACC GCC TACATACCTC GCTCTGCTAA 2640
 TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG TTGGACTCAA 2700
 GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC GGGGGGTTCG TGCACACAGC 2760
 CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT ACAGCGTGAG CTATGAGAAA 2820
 GCGCCACGCT TCCGAAAGGG AGAAAGGCGG ACAGGTATCC GGTAAGCGGC AGGTCGGAA 2880
 CAGGAGAGCG CACGAGGGAG CTTCAGGGG GAAACGCCTG GTATCTTTAT AGTCTGTGCG 2940
 GGTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG GGGCGGAGCC 3000
 TATGGA AAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT GGCCTTTTGC TGGCCTTTTG 3060
 CTCACATGTT CTTTCTGCG TTATCCCTG ATTCTGTGGA TAACCGTATT ACCGCCTTTG 3120
 AGTGAGCTGA TACCGCTCGC CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG 3180
 AAGCGGAAGA 3190

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide (NLC95)
 used to analyze products of transposition."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATAATCCTTA AAAACTCCAT TTCCACCCCT 30

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide (NLC209)
 used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGATTGCAC CGATCTTCTA CACCGTTCC

29

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide (NLC429) used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCACCGTC ATCACCGAAA CGCGCGAGAC

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide (NLC430) used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATGACTTGG TTGAGTACTC ACCAGTCACA

30

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide (NLC431) used to analyze the products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAACGAAA TAGACAGATC GCTGAGATAG

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide (NLC432)
used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAAGACGATA GTTACCGGAT AAGGCGCAGC

30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide (NLC94)
used for sequence determination"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAGTCCAGT ATGCTTTTTC ACAGCATAAC

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Tyr Asn Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:15:

Category	Sub-category	Value	Unit
Energy	Electricity	100	kWh
	Gas	100	kWh
Water	Hot water	100	kWh
	Cold water	100	kWh
Waste	Recycling	100	kWh
	Landfill	100	kWh
Transport	Car	100	kWh
	Bus	100	kWh
Communication	Internet	100	kWh
	Mobile phone	100	kWh
Healthcare	Hospital	100	kWh
	Pharmacy	100	kWh
Education	School	100	kWh
	University	100	kWh
Government	City hall	100	kWh
	National government	100	kWh
Retail	Supermarket	100	kWh
	Department store	100	kWh
Finance	Bank	100	kWh
	Insurance company	100	kWh
Media	Newspaper	100	kWh
	Magazine	100	kWh
Food	Restaurant	100	kWh
	Fast food	100	kWh
Housing	Apartment	100	kWh
	House	100	kWh
Transportation	Train	100	kWh
	Subway	100	kWh
Healthcare	Physician	100	kWh
	Nurse	100	kWh
Education	Teacher	100	kWh
	Student	100	kWh
Government	Police officer	100	kWh
	Firefighter	100	kWh
Retail	Shop assistant	100	kWh
	Customer	100	kWh
Finance	Banker	100	kWh
	Investor	100	kWh
Media	Journalist	100	kWh
	Editor	100	kWh
Food	Chef	100	kWh
	Waiter	100	kWh
Housing	Landlord	100	kWh
	Tenant	100	kWh
Transportation	Driver	100	kWh
	Passenger	100	kWh
Healthcare	Doctor	100	kWh
	Pharmacist	100	kWh
Education	Professor	100	kWh
	Researcher	100	kWh
Government	Mayor	100	kWh
	Minister	100	kWh
Retail	Manager	100	kWh
	Employee	100	kWh
Finance	Analyst	100	kWh
	Trader	100	kWh
Media	Reporter	100	kWh
	Producer	100	kWh
Food	Owner	100	kWh
	Staff	100	kWh
Housing	Owner	100	kWh
	Manager	100	kWh
Transportation	Owner	100	kWh
	Operator	100	kWh
Healthcare	Owner	100	kWh
	Manager	100	kWh
Education	Owner	100	kWh
	Manager	100	kWh
Government	Owner	100	kWh
	Manager	100	kWh
Retail	Owner	100	kWh
	Manager	100	kWh
Finance	Owner	100	kWh
	Manager	100	kWh
Media	Owner	100	kWh
	Manager	100	kWh
Food	Owner	100	kWh
	Manager	100	kWh
Housing	Owner	100	kWh
	Manager	100	kWh
Transportation	Owner	100	kWh
	Manager	100	kWh
Healthcare	Owner	100	kWh
	Manager	100	kWh
Education	Owner	100	kWh
	Manager	100	kWh
Government	Owner	100	kWh
	Manager	100	kWh
Retail	Owner	100	kWh
	Manager	100	kWh
Finance	Owner	100	kWh
	Manager	100	kWh
Media	Owner	100	kWh
	Manager	100	kWh
Food	Owner	100	kWh
	Manager	100	kWh
Housing	Owner	100	kWh
	Manager	100	kWh
Transportation	Owner	100	kWh
	Manager	100	kWh
Healthcare	Owner	100	kWh
	Manager	100	kWh
Education	Owner	100	kWh
	Manager	100	kWh
Government	Owner	100	kWh
	Manager	100	kWh
Retail	Owner	100	kWh
	Manager	100	kWh
Finance	Owner	100	kWh
	Manager	100	kWh
Media	Owner	100	kWh
	Manager	100	kWh
Food	Owner	100	kWh
	Manager	100	kWh

[illegible][illegible]

	Pre-Test	Post-Test	Improvement
Mean	70.86	90.86	20
Standard Deviation	10.25	10.25	0
N	10	10	0